

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/421,971

DATE: 06/27/2001  
TIME: 15:18:57

Input Set : A:\SALK2350.ST25.txt  
Output Set: N:\CRF3\06272001\I421971.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: GAGE, Fred  
4 SUHR, Steven  
5 GIL, Elad  
6 SENUT, Marie-Claude  
8 <120> TITLE OF INVENTION: HORMONE RECEPTOR FUNCTIONAL DIMERS AND METHODS OF THEIR USE  
10 <130> FILE REFERENCE: SALK2350  
12 <140> CURRENT APPLICATION NUMBER: US 09/421,971  
13 <141> CURRENT FILING DATE: 1999-10-20  
15 <160> NUMBER OF SEQ ID NOS: 75  
17 <170> SOFTWARE: PatentIn version 3.0

#### ERRORED SEQUENCES

254 <210> SEQ ID NO: 14  
255 <211> LENGTH: 13  
256 <212> TYPE: DNA  
257 <213> ORGANISM: Artificial Sequence  
259 <220> FEATURE:  
260 <221> NAME/KEY: misc\_feature  
261 <223> OTHER INFORMATION: Nucleotide encoding SfiI recognition site  
263 <220> FEATURE:  
264 <221> NAME/KEY: misc\_feature  
265 <222> LOCATION: (5)..(9)  
266 <223> OTHER INFORMATION: n is either g, t, c, or a  
268 <400> SEQUENCE: 14  
E--> 270 ggccnnnnng gcc 13 *format error*  
271 13  
326 <210> SEQ ID NO: 18  
327 <211> LENGTH: 41  
328 <212> TYPE: DNA  
329 <213> ORGANISM: Artificial Sequence  
331 <220> FEATURE:  
332 <221> NAME/KEY: misc\_feature  
333 <223> OTHER INFORMATION: hRXR N-terminal SfiI primer 5'  
335 <400> SEQUENCE: 18  
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338 41  
341 <210> SEQ ID NO: 19  
342 <211> LENGTH: 20  
343 <212> TYPE: DNA  
344 <213> ORGANISM: Artificial Sequence  
346 <220> FEATURE:  
347 <221> NAME/KEY: misc\_feature  
348 <223> OTHER INFORMATION: hRXR N-terminal SfiI primer 3'  
350 <400> SEQUENCE: 19  
E--> 352 gatgggggag ctcaggggtgc *same*

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353 20  
356 <210> SEQ ID NO: 20  
357 <211> LENGTH: 22  
358 <212> TYPE: DNA  
359 <213> ORGANISM: Artificial Sequence  
361 <220> FEATURE:  
362 <221> NAME/KEY: misc\_feature  
363 <223> OTHER INFORMATION: hRXR C-terminal SfiI primer 5'  
365 <400> SEQUENCE: 20  
E--> 367 ggagagctcg aggccctactg ca  
368 22  
371 <210> SEQ ID NO: 21  
372 <211> LENGTH: 39  
373 <212> TYPE: DNA  
374 <213> ORGANISM: Artificial Sequence  
376 <220> FEATURE:  
377 <221> NAME/KEY: misc\_feature  
378 <223> OTHER INFORMATION: hRXR C-terminal SfiI primer 3'  
380 <400> SEQUENCE: 21  
E--> 382 accatcgatt cagggccctg ttggcccggtg cggcgccctc  
383 39  
386 <210> SEQ ID NO: 22  
387 <211> LENGTH: 41  
388 <212> TYPE: DNA  
389 <213> ORGANISM: Artificial Sequence  
391 <220> FEATURE:  
392 <221> NAME/KEY: misc\_feature  
393 <223> OTHER INFORMATION: dmusp N-terminal SfiI primer 5'  
395 <400> SEQUENCE: 22  
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398 41  
401 <210> SEQ ID NO: 23  
402 <211> LENGTH: 20  
403 <212> TYPE: DNA  
404 <213> ORGANISM: Artificial Sequence  
406 <220> FEATURE:  
407 <221> NAME/KEY: misc\_feature  
408 <223> OTHER INFORMATION: dmusp N-terminal SfiI primer 3'  
410 <400> SEQUENCE: 23  
E--> 412 cagcacgtgg accattgaca  
413 20  
416 <210> SEQ ID NO: 24  
417 <211> LENGTH: 24  
418 <212> TYPE: DNA  
419 <213> ORGANISM: Artificial Sequence  
421 <220> FEATURE:  
422 <221> NAME/KEY: misc\_feature  
423 <223> OTHER INFORMATION: dmusp C-terminal SfiI primer 5'  
425 <400> SEQUENCE: 24

*done*  
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E--> 427 ggagagctct ttctcgagca gctg  
428 24  
431 <210> SEQ ID NO: 25  
432 <211> LENGTH: 49  
433 <212> TYPE: DNA  
434 <213> ORGANISM: Artificial Sequence  
436 <220> FEATURE:  
437 <221> NAME/KEY: misc\_feature  
438 <223> OTHER INFORMATION: dmusp C-terminal SfiI primer 3'  
440 <400> SEQUENCE: 25  
E--> 442 accatcgatt caggccctg ttggccctc cagtttcatc gccaggccg  
443 49  
446 <210> SEQ ID NO: 26  
447 <211> LENGTH: 36  
448 <212> TYPE: DNA  
449 <213> ORGANISM: Artificial Sequence  
451 <220> FEATURE:  
452 <221> NAME/KEY: misc\_feature  
453 <223> OTHER INFORMATION: VP16 N-terminal SfiI primer 5'  
455 <400> SEQUENCE: 26  
E--> 457 cataagctta tgggacagac actgatggga cggccc  
458 36  
461 <210> SEQ ID NO: 27  
462 <211> LENGTH: 31  
463 <212> TYPE: DNA  
464 <213> ORGANISM: Artificial Sequence  
466 <220> FEATURE:  
467 <221> NAME/KEY: misc\_feature  
468 <223> OTHER INFORMATION: VP16 N-terminal SfiI primer 3'  
470 <400> SEQUENCE: 27  
E--> 472 cagagaccat gggccctgtt ggccccccac c  
473 31  
476 <210> SEQ ID NO: 28  
477 <211> LENGTH: 18  
478 <212> TYPE: DNA  
479 <213> ORGANISM: Artificial Sequence  
481 <220> FEATURE:  
482 <221> NAME/KEY: misc\_feature  
483 <223> OTHER INFORMATION: VP16 C-terminal SfiI primer 5'  
485 <400> SEQUENCE: 28  
E--> 487 ttaccgctag ctccacca  
488 18  
491 <210> SEQ ID NO: 29  
492 <211> LENGTH: 36  
493 <212> TYPE: DNA  
494 <213> ORGANISM: Artificial Sequence  
496 <220> FEATURE:  
497 <221> NAME/KEY: misc\_feature  
498 <223> OTHER INFORMATION: VP16 C-terminal SfiI primer 3'

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Input Set : A:\SALK2350.ST25.txt  
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500 <400> SEQUENCE: 29  
E--> 502 gtagatatca gggccctgtt ggcccaagtgc tcgagt  
503 36  
506 <210> SEQ ID NO: 30  
507 <211> LENGTH: 36  
508 <212> TYPE: DNA  
509 <213> ORGANISM: Artificial Sequence  
511 <220> FEATURE:  
512 <221> NAME/KEY: misc\_feature  
513 <223> OTHER INFORMATION: Annealing two linker encoding oligonucleotides 5'  
515 <400> SEQUENCE: 30  
E--> 517 gggccaggag gtggctccgg gggaggttca ggcaca  
518 36  
521 <210> SEQ ID NO: 31  
522 <211> LENGTH: 36  
523 <212> TYPE: DNA  
524 <213> ORGANISM: Artificial Sequence  
526 <220> FEATURE:  
527 <221> NAME/KEY: misc\_feature  
528 <223> OTHER INFORMATION: Annealing two linker encoding oligonucleotides 3'  
530 <400> SEQUENCE: 31  
E--> 532 gcctgaacct ccccccggagc cacccctcgg ccctgt  
533 36  
536 <210> SEQ ID NO: 32  
537 <211> LENGTH: 47  
538 <212> TYPE: DNA  
539 <213> ORGANISM: Artificial Sequence  
541 <220> FEATURE:  
542 <221> NAME/KEY: misc\_feature  
543 <223> OTHER INFORMATION: F-domain deleted ecdysone receptor fragment polylinker 5'  
545 <400> SEQUENCE: 32  
E--> 547 aagcttgaga gatctgggac ggccggccgg gggctagcgg gccaaca  
548 47

*Name*  
↓

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/421,971

DATE: 06/27/2001

TIME: 15:18:58

Input Set : A:\SALK2350.ST25.txt

Output Set: N:\CRF3\06272001\I421971.raw

L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:270 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:13 SEQ:14  
L:337 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:18  
L:352 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:19  
L:367 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:20  
L:382 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:21  
L:397 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:22  
L:412 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:23  
L:427 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:24  
L:442 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:49 SEQ:25  
L:457 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:26  
L:472 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:27  
L:487 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:28  
L:502 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:29  
L:517 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:30  
L:532 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:31  
L:547 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:47 SEQ:32